

1653

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,978A

DATE: 06/28/2002

TIME: 11:05:41

Input Set : A:\57961.app

Output Set: N:\CRF3\06282002\I647978A.raw

3 <110> APPLICANT: Warner-Lambert Company
 5 <120> TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein
 7 <130> FILE REFERENCE: 09/647,978
 9 <140> CURRENT APPLICATION NUMBER: 09/647,978A
 10 <141> CURRENT FILING DATE: 2000-10-06
 12 <150> PRIOR APPLICATION NUMBER: PCT/US99/08568
 13 <151> PRIOR FILING DATE: 1999-04-19
 15 <150> PRIOR APPLICATION NUMBER: 60/082,454
 16 <151> PRIOR FILING DATE: 1998-04-20
 18 <160> NUMBER OF SEQ ID NOS: 6
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1674
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Mouse
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 30 aggaatgaag gaccgctgggt gtatattcat gaagtcattc ctggaggtga ctgttacaag 180
 31 gatggacgtt tgaagccagg agatcaactt gtctcaataaa acaaggaatc tatgatttgt 240
 32 gtatcatttg aagaagcaaa aacgataatt accagagcca agttgagggtc agaatctccc 300
 33 tgggagatag cattcatcag aaaaaagtct tacttgccat atccaggaaa tatttgctgt 360
 34 ccatccccac aagtgtcaga agactgtgga cctcaaacct caacatttac tcttcttcc 420
 35 ttcctcttgc aaacactact tccaaagact tcataccatc cccagactca ggactccact 480
 36 ttcccttctt gtaaaagcaat tcagacaaaaa cctgaacacg ataaaacaga acatagtcca 540
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 38 actgatgatg attctggacc acaaggaaag atttccctaa atccttctgt tcgccttaag 660
 39 gcagagaaac tggaaatggc tctcaattac ctggatatac aqccaacaaa ggaacaacgt 720
 40 gaagccctga gagagcaagt ccaggccgac tcaaaggaaa ctgtgtcttt tggagatttc 780
 41 gtccaggtt ccagaagttt gtttgcattt cagttggatg aagtaatgt tgggttccat 840
 42 gaaatccccca gcatcttgc ttcacagctt ctccctgtt attctctaga agcagatgaa 900
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 45 caggaagccca aagctgttagc tgaggaaacc cgagctctgc gaagccggat tcatctcgca 1080
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 63 <400> SEQUENCE: 2
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 70 Leu Lys Ile Leu Gly Gly Ile Asn Arg Asn Glu Gly Pro Leu Val Tyr
 35 40 45
 73 Ile His Glu Val Ile Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu
 50 55 60
 76 Lys Pro Gly Asp Gln Leu Val Ser Ile Asn Lys Glu Ser Met Ile Gly
 65 70 75 80
 79 Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg
 80 85 90 95
 82 Ser Glu Ser Pro Trp Glu Ile Ala Phe Ile Arg Gln Lys Ser Tyr Cys
 100 105 110
 85 Gly His Pro Gly Asn Ile Cys Cys Pro Ser Pro Gln Val Ser Glu Asp
 115 120 125
 88 Cys Gly Pro Gln Thr Ser Thr Phe Thr Leu Leu Ser Ser Pro Ser Glu
 130 135 140
 91 Thr Leu Leu Pro Lys Thr Ser Ser Thr Pro Gln Thr Gln Asp Ser Thr
 145 150 155 160
 94 Phe Pro Ser Cys Lys Ala Ile Gln Thr Lys Pro Glu His Asp Lys Thr
 165 170 175
 97 Glu His Ser Pro Ile Thr Ser Leu Asp Asn Ser Pro Ala Asp Thr Ser
 180 185 190
 100 Asn Ala Asp Ile Ala Pro Ala Trp Thr Asp Asp Asp Ser Gly Pro Gln
 195 200 205
 103 Gly Lys Ile Ser Leu Asn Pro Ser Val Arg Leu Lys Ala Glu Lys Leu
 210 215 220
 106 Glu Met Ala Leu Asn Tyr Leu Gly Ile Gln Pro Thr Lys Glu Gln Arg
 225 230 235 240
 109 Glu Ala Leu Arg Glu Gln Val Gln Ala Asp Ser Lys Gly Thr Val Ser
 245 250 255
 112 Phe Gly Asp Phe Val Gln Val Ala Arg Ser Leu Phe Cys Leu Gln Leu
 260 265 270
 115 Asp Glu Val Asn Val Gly Val His Glu Ile Pro Ser Ile Leu Asp Ser
 275 280 285
 118 Gln Leu Leu Pro Cys Asp Ser Leu Glu Ala Asp Glu Val Gly Lys Leu
 290 295 300
 121 Arg Gln Glu Arg Asn Ala Ala Leu Glu Glu Arg Asn Val Leu Lys Glu
 305 310 315 320
 124 Lys Leu Leu Glu Ser Glu Lys His Arg Lys Gln Leu Ile Glu Glu Leu
 325 330 335
 127 Gln Asn Val Lys Gln Glu Ala Lys Ala Val Ala Glu Glu Thr Arg Ala

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130	Leu Arg Ser Arg Ile His Leu Ala Glu Ala Ala Gln Arg Gln Ala His		
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133	Gly Met Glu Met Asp Tyr Glu Glu Val Ile Arg Leu Leu Glu Ala Glu		
134	370	375	380
136	Val Ser Glu Leu Lys Ala Gln Leu Ala Asp Tyr Ser Asp Gln Asn Lys		
137	385	390	395
139	Glu Ser Val Gln Asp Leu Arg Lys Arg Val Thr Val Leu Asp Cys Gln		400
140	405	410	415
142	Leu Arg Lys Ser Glu Met Ala Arg Lys Ala Phe Lys Ala Ser Thr Glu		
143	420	425	430
145	Arg Leu Leu Gly Phe Ile Glu Ala Ile Gln Glu Val Leu Leu Asp Ser		
146	435	440	445
148	Ser Ala Pro Leu Ser Thr Leu Ser Glu Arg Arg Ala Val Leu Ala Ser		
149	450	455	460
151	Gln Thr Ser Leu Pro Leu Leu Ala Arg Asn Gly Arg Ser Phe Pro Ala		
152	465	470	475
154	480	485	495
157	Thr Leu Leu Leu Glu Ser Lys Glu Leu Val Arg Ser Val Arg Ala Ile		
158	500	505	510
160	Asp Gly Ile Lys Tyr Phe Ile Asn His Val Thr Gln Thr Thr Ser Trp		
161	515	520	525
163	Ile His Pro Val Met Ser Ala Leu Asn Leu Ser Cys Ala Glu Glu Ser		
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178	ttggaaaaga agaatttcta gactcttcata caagatcttcc atttatacag ctgttaatc 180		
179	caaggctact ttggtaaaag catgaataaa aatacatcta ctgttagtac acccagtcta 240		
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183	aacaaggaat ctatgattgg ttttatcattt gaagaagccaa aaagcataat taccagagcc 480		
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187	actccccaaa caaataatga cattttatct tcttgtgaga taaaaactgg atacaacaaa 720		
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191	gaacaacacc aagcccttag acagcaagta caagcagact caaaaggac agtgtcttt 960		
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193 ggtcacatg aaatttccaa tatatttagat tcacagcttc ttcccttgta ttcttcagaa 1080
 194 gcagatgaaa tggaaaggct caagtgtcaa agagatgatg ccttgaaga agtaaaataca 1140
 195 cttaggaaaa aattatttgcg atcagataag caaaggaaac aattgacaga agagctccag 1200
 196 aatgtgaaac aagaagccaa agctgttagtt gaagaaaacaa gagccctgcg tagtcggatt 1260
 197 catcttgctg aagctgctca gagacaggca catggaatgg aatggacta tgaagaagtg 1320
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 207 tggatgtttt ccttaggaag tggagctaca tggatgtatgt gaggcagagac gcataacatc 1920
 208 caattcttagt atgaaacagt ctaaaatagg agttaaagcat gcactactt tttttttttt 1980
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 221 cggaaatgaaat gcccatttgtt atatatttgcg gaaattatttgcg tggaggaga ctgttataag 180
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 224 tggagatag cattcataag aaaaaatcc gacaacattt agccagaaaaa tctgtcatgt 360
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245 actacatccct ggatccatcc cgtgatgagt gtcctgaatc tatctcgctc agaggagaat 1620
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 262 35 40 45
 264 Ile Gln Glu Ile Ile Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu
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 267 Lys Pro Gly Asp Gln Leu Val Ser Val Asn Lys Glu Ser Met Ile Gly
 268 65 70 75 80
 270 Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg
 271 85 90 95
 273 Leu Glu Ser Ala Trp Glu Ile Ala Phe Ile Arg Gln Lys Ser Asp Asn
 274 100 105 110
 276 Ile Gln Pro Glu Asn Leu Ser Cys Thr Ser Leu Ile Glu Ala Ser Gly
 277 115 120 125
 279 Glu Tyr Gly Pro Gln Ala Ser Thr Leu Ser Leu Phe Ser Ser Pro Pro
 280 130 135 140
 282 Glu Ile Leu Ile Pro Lys Thr Ser Ser Thr Pro Lys Thr Asn Asn Asp
 283 145 150 155 160
 285 Ile Leu Ser Ser Cys Glu Ile Lys Thr Gly Tyr Asn Lys Thr Val Gln
 286 165 170 175
 288 Ile Pro Ile Thr Ser Glu Asn Ser Thr Val Gly Leu Ser Asn Thr Asp
 289 180 185 190
 291 Val Ala Ser Ala Trp Thr Glu Asn Tyr Gly Leu Gln Glu Lys Ile Ser
 292 195 200 205
 294 Leu Asn Pro Ser Val Arg Phe Lys Ala Glu Lys Leu Glu Met Ala Leu
 295 210 215 220
 297 Asn Tyr Leu Gly Ile Gln Pro Thr Lys Glu Gln His Gln Ala Leu Arg
 298 225 230 235 240
 300 Gln Gln Val Gln Ala Asp Ser Lys Gly Thr Val Ser Phe Gly Asp Phe
 301 245 250 255
 303 Val Gln Val Ala Arg Asn Leu Phe Cys Leu Gln Leu Asp Glu Val Asn
 304 260 265 270
 306 Val Gly Ala His Glu Ile Ser Asn Ile Leu Asp Ser Gln Leu Leu Pro
 307 275 280 285
 309 Cys Asp Ser Ser Glu Ala Asp Glu Met Glu Arg Leu Lys Cys Glu Arg
 310 290 295 300
 312 Asp Asp Ala Leu Lys Glu Val Asn Thr Leu Lys Glu Lys Leu Leu Glu
 313 305 310 315 320
 315 Ser Asp Lys Gln Arg Lys Gln Leu Thr Glu Glu Leu Gln Asn Val Lys
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VERIFICATION SUMMARY
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